Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expect: 10.000   wordsize: 11   Filter ☑   View option Standard ▼
Masking character option X for protein, n for nucleotide ▼   Masking color option Black ▼
☐ Show CDS translation   Align

Sequence 1: lcl|1
Length = 1268 (1 .. 1268)

Sequence 2: gi|22797892|Xenopus laevis mRNA for endoU protein >gi|148222782|ref|NM_001087571.1| Xenopus
laevis endoribonuclease endoU (endou-A), mRNA
Length = 1268 (1 .. 1268)
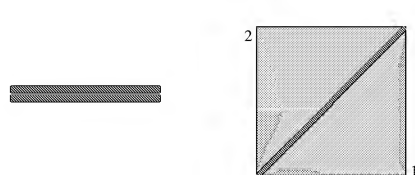
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 2404 bits (1250),  Expect = 0.0
 Identities = 1268/1268 (100%),  Gaps = 0/1268 (0%)
 Strand=Plus/Plus

Query  1    ATTGGGGAACTGGGAGCAGAGAGTGACGGGCAGGAGCCATGGCGAGTAACAGGGGGCAGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATTGGGGAACTGGGAGCAGAGAGTGACGGGCAGGAGCCATGGCGAGTAACAGGGGGCAGC  60

Query  61   TGAACCATGAACTCTCCAAGCTGTTTAATGAGCTGTGGGACGCAGATCAGAACCGGATGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGAACCATGAACTCTCCAAGCTGTTTAATGAGCTGTGGGACGCAGATCAGAACCGGATGA  120

Query  121  AGTCCGGGAAGGATTATCGGATCTCCTTGCAGGGTAAAGCAGGGTACGTACCCGCCGGTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTCCGGGAAGGATTATCGGATCTCCTTGCAGGGTAAAGCAGGGTACGTACCCGCCGGTT  180

Query  181  CCAACCAGGCCAGGGACAGCAGCGCCTCGGTTCCCGCTCTTCCAGTTCGTCGATGAGGAGAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCAACCAGGCCAGGGACAGCAGCGCCTCGGTTCCCGCTCTTCCAGTTCGTCGATGAGGAGAAGC  240
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Query  241   TGAAGAGCAGGAAGACGTTTGCAACCTTCATTTCCCTGCTGGACAATTATGAGATGGACA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TGAAGAGCAGGAAGACGTTTGCAACCTTCATTTCCCTGCTGGACAATTATGAGATGGACA   300

Query  301   CGGGGGTGGCCGAGGTTGTGACTCCGGAGGAAATCGCTGAAAACAACAACTTCCTGGACG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CGGGGGTGGCCGAGGTTGTGACTCCGGAGGAAATCGCTGAAAACAACAACTTCCTGGACG   360

Query  361   CCATTCTGGAAACCAAAGTGATGAAGATGGCACATGACTACCTGGTGAGGAAGAACCAAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCATTCTGGAAACCAAAGTGATGAAGATGGCACATGACTACCTGGTGAGGAAGAACCAAG   420

Query  421   CCAAACCCCACCCGGAATGACTTCAAGGTCCAACTGTACAACATCTGGTTCCAGCTGTACT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CCAAACCCCACCCGGAATGACTTCAAGGTCCAACTGTACAACATCTGGTTCCAGCTGTACT   480

Query  481   CACGGGCCCCAGGGAGCAGACCCGATTCGTGCGGCTTTGAGCACGTGTTTGTGGGAGAAT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CACGGGCCCCAGGGAGCAGACCCGATTCGTGCGGCTTTGAGCACGTGTTTGTGGGAGAAT   540

Query  541   CGAAGCGAGGGCAGGAGATGATGGGGCTTCACAACTGGGTCCAGTTTTACCTTCAGGAGA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CGAAGCGAGGGCAGGAGATGATGGGGCTTCACAACTGGGTCCAGTTTTACCTTCAGGAGA   600

Query  601   AGAGGAAGAACATCGACTATAAAGGATACGTGGCTCGGCAGAACAAGAGTCGGCCGGATG   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   AGAGGAAGAACATCGACTATAAAGGATACGTGGCTCGGCAGAACAAGAGTCGGCCGGATG   660

Query  661   AAGATGATCAGGTGTTGAACCTGCAGTTCAATTGGAAGGAGATGGTGAAACCCGTCGGCA   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   AAGATGATCAGGTGTTGAACCTGCAGTTCAATTGGAAGGAGATGGTGAAACCCGTCGGCA   720

Query  721   GCAGCTTCATTGGCGTCAGCCCGGAATTCGAATTCGCCCTTTACACCATCGTCTTCCTCG   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   GCAGCTTCATTGGCGTCAGCCCGGAATTCGAATTCGCCCTTTACACCATCGTCTTCCTCG   780

Query  781   CGTCTCAGGAGAAGATGAGCCGAGAAGTCGTTCGGCTGGAAGAATACGAACTGCAGATCG   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   CGTCTCAGGAGAAGATGAGCCGAGAAGTCGTTCGGCTGGAAGAATACGAACTGCAGATCG   840

Query  841   TCGTCAATCGCCACGGCCGTTATATAGGGACCGCCTACCCCGTCCTCCTGAGCACCAATA   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   TCGTCAATCGCCACGGCCGTTATATAGGGACCGCCTACCCCGTCCTCCTGAGCACCAATA   900

Query  901   ACCCGGATCTGTACTGAGGGGGCGGGGCTAGAGATCACAGCCGGTTCCCACGGTTTGGGT   960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   ACCCGGATCTGTACTGAGGGGGCGGGGCTAGAGATCACAGCCGGTTCCCACGGTTTGGGT   960

Query  961   GCATTTACTAACAAAACTGCACCAATGCAACAACAATGCAAGCAGATAATGGGGGCAGGT   1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961   GCATTTACTAACAAAACTGCACCAATGCAACAACAATGCAAGCAGATAATGGGGGCAGGT   1020

Query  1021  CCATATCCCTCTGCTTTCCCTAGCGTGTGTGGGGCACATTAACCCTATAACTGTCACTCA   1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021  CCATATCCCTCTGCTTTCCCTAGCGTGTGTGGGGCACATTAACCCTATAACTGTCACTCA   1080

Query  1081  CTGCACCAGACCCATTATTTAACCCCACAAGGGACATCAAGCCAGTGCCTTGTTATGAGA   1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  CTGCACCAGACCCATTATTTAACCCCACAAGGGACATCAAGCCAGTGCCTTGTTATGAGA   1140

Query  1141  GAGCGCAGCCGGGGCTTCTCTACTGTGAAACTTCTGTATTGTATAGAGTTTACTTGGTTT   1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  GAGCGCAGCCGGGGCTTCTCTACTGTGAAACTTCTGTATTGTATAGAGTTTACTTGGTTT   1200

Query  1201  CTTCATCCAGACAATTTCACTTTTTTTTTGCTTTGCCTTTAACCATTAAAAGTCCATGAC   1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1201  CTTCCTCCAGACAATTTCACTTTTTTTTTGCTTTGCCTTTAACCATTAAAAGTCCATGAC  1260

Query  1261  ATTTCTGT  1268
             ||||||||
Sbjct  1261  ATTTCTGT  1268
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CPU time:     0.04 user secs.        0.04 sys. secs        0.08 total secs.
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